

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/524,970A  
Source: 1Fw/b  
Date Processed by STIC: 6/14/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 06/14/2006

PATENT APPLICATION: US/10/524,970A

TIME: 09:28:22

Input Set : A:\62870702.APP

Output Set: N:\CRF4\06142006\J524970A.raw

3 <110> APPLICANT: IRIMURA, TATSURO  
 4 MAENUMA, KEISUKE  
 5 KOMATSU, KUNIMITSU  
 6 TACHIKI, AYUMI  
 7 MATSUMOTO, MARIKO  
 9 <120> TITLE OF INVENTION: USE OF LECTIN LIBRARY FOR DISTINGUISHING GLYCOPROTEINS  
 10 OR CELLS, DIAGNOSING SERUM OR CELLS, OR FRACTIONATING  
 11 GLYCOPROTEINS OR CELLS  
 13 <130> FILE REFERENCE: 62870(70232)  
 15 <140> CURRENT APPLICATION NUMBER: 10/524,970A  
 16 <141> CURRENT FILING DATE: 2005-08-18  
 18 <150> PRIOR APPLICATION NUMBER: PCT/JP03/10461  
 19 <151> PRIOR FILING DATE: 2003-08-19  
 21 <150> PRIOR APPLICATION NUMBER: JP 2002-239979  
 22 <151> PRIOR FILING DATE: 2002-08-20  
 24 <160> NUMBER OF SEQ ID NOS: 40  
 26 <170> SOFTWARE: PatentIn Ver. 3.3  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 950  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Maackia amurensis  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: CDS  
 35 <222> LOCATION: (4)..(858)  
 37 <400> SEQUENCE: 1  
 38 gcc atg gct act tcc aac tca aaa cca act caa gtc ctt ctt gcc acc 48  
 39 Met Ala Thr Ser Asn Ser Lys Pro Thr Gln Val Leu Leu Ala Thr  
 40 1 5 10 15  
 42 ttc tta act ttc ttc ctt ttg cta ctc aac aac gta aac tca tca gat 96  
 43 Phe Leu Thr Phe Phe Leu Leu Leu Leu Asn Val Asn Ser Ser Asp  
 44 20 25 30  
 46 gag ctt tct ttt acc atc aac aat ttc atg cca aat caa ggc gat cta 144  
 47 Glu Leu Ser Phe Thr Ile Asn Asn Phe Met Pro Asn Gln Gly Asp Leu  
 48 35 40 45  
 50 ctc ttc caa ggt gta gcc act gtt tca cca aca ggg gta tta caa ctt 192  
 51 Leu Phe Gln Gly Val Ala Thr Val Ser Pro Thr Gly Val Leu Gln Leu  
 52 50 55 60  
 54 acc agc gaa gaa aac ggt caa ccc ctg gag tat tct gtt ggc aga gct 240  
 55 Thr Ser Glu Glu Asn Gly Gln Pro Leu Glu Tyr Ser Val Gly Arg Ala  
 56 65 70 75  
 58 cta tat act gcc cct gtg cgc att tgg gac agt acc act ggc gcc gta 288  
 59 Leu Tyr Thr Ala Pro Val Arg Ile Trp Asp Ser Thr Thr Gly Ala Val  
 60 80 85 90 95

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```

62 gca agc ttc tcc act tcc ttc acc ttt gtt gtg aaa gca gct agg gga 336
63 Ala Ser Phe Ser Thr Ser Phe Thr Phe Val Val Lys Ala Ala Arg Gly
64      100      105      110
66 gct tct gac ggt tta gcc ttc ttt ctt gca cca cct gat tct cag atc 384
67 Ala Ser Asp Gly Leu Ala Phe Phe Leu Ala Pro Pro Asp Ser Gln Ile
68      115      120      125
70 cct tcg ggc agc gta tcg aaa tac cta gga ctt ttt aac aac tca aat 432
71 Pro Ser Gly Ser Val Ser Lys Tyr Leu Gly Leu Phe Asn Asn Ser Asn
72      130      135      140
74 tcc gat agt tcc aac caa att gtt gct gta gag ttt gac act tac ttc 480
75 Ser Asp Ser Ser Asn Gln Ile Val Ala Val Glu Phe Asp Thr Tyr Phe
76      145      150      155
78 ggc cat agt tat gat ccc tgg gat cca aat tat cga cat atc gga att 528
79 Gly His Ser Tyr Asp Pro Trp Asp Pro Asn Tyr Arg His Ile Gly Ile
80 160      165      170      175
82 gat gtc aac ggt att gag tcg ata aaa act gtg caa tgg gat tgg att 576
83 Asp Val Asn Gly Ile Glu Ser Ile Lys Thr Val Gln Trp Asp Trp Ile
84      180      185      190
86 aac ggc gga gtt gcc ttt gct acc ata acc tat cta gct ccc aac aaa 624
87 Asn Gly Gly Val Ala Phe Ala Thr Ile Thr Tyr Leu Ala Pro Asn Lys
88      195      200      205
90 acg tta ata gca tct cta gtt tac cct tcc aat caa aca agt ttc att 672
91 Thr Leu Ile Ala Ser Leu Val Tyr Pro Ser Asn Gln Thr Ser Phe Ile
92      210      215      220
94 gtc gct gct tct gtt gat ttg aag gga atc ctc cct gag tgg gtt aga 720
95 Val Ala Ala Ser Val Asp Leu Lys Gly Ile Leu Pro Glu Trp Val Arg
96      225      230      235
98 gtt ggt ttc tct gct gcc acg ggt gct cct aaa gca gtt gaa acc cac 768
99 Val Gly Phe Ser Ala Ala Thr Gly Ala Pro Lys Ala Val Glu Thr His
100 240      245      250      255
102 gat gtt cgt tcc tgg tct ttc acg tca act ttg gaa gcc aac agc cct 816
103 Asp Val Arg Ser Trp Ser Phe Thr Ser Thr Leu Glu Ala Asn Ser Pro
104      260      265      270
106 gct gat gtg gat aat aat gtg cat atc gca cgt tac act gca 858
107 Ala Asp Val Asp Asn Asn Val His Ile Ala Arg Tyr Thr Ala
108      275      280      285
110 tgatctcgtg agcttttcgta tgtattaggt gtttatgtaa attaaataaaa aatgacctga 918
112 aataatgggt atcggcgcag ctatacaaaa at 950
115 <210> SEQ ID NO: 2
116 <211> LENGTH: 285
117 <212> TYPE: PRT
118 <213> ORGANISM: Maackia amurensis
120 <400> SEQUENCE: 2
121 Met Ala Thr Ser Asn Ser Lys Pro Thr Gln Val Leu Leu Ala Thr Phe
122 1 5 10 15
124 Leu Thr Phe Phe Leu Leu Leu Leu Asn Asn Val Asn Ser Ser Asp Glu
125 20 25 30
127 Leu Ser Phe Thr Ile Asn Asn Phe Met Pro Asn Gln Gly Asp Leu Leu
128 35 40 45

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130 Phe Gln Gly Val Ala Thr Val Ser Pro Thr Gly Val Leu Gln Leu Thr
131      50                      55                      60
133 Ser Glu Glu Asn Gly Gln Pro Leu Glu Tyr Ser Val Gly Arg Ala Leu
134 65                      70                      75                      80
136 Tyr Thr Ala Pro Val Arg Ile Trp Asp Ser Thr Thr Gly Ala Val Ala
137                      85                      90                      95
139 Ser Phe Ser Thr Ser Phe Thr Phe Val Val Lys Ala Ala Arg Gly Ala
140                      100                      105                      110
142 Ser Asp Gly Leu Ala Phe Phe Leu Ala Pro Pro Asp Ser Gln Ile Pro
143                      115                      120                      125
145 Ser Gly Ser Val Ser Lys Tyr Leu Gly Leu Phe Asn Asn Ser Asn Ser
146                      130                      135                      140
148 Asp Ser Ser Asn Gln Ile Val Ala Val Glu Phe Asp Thr Tyr Phe Gly
149 145                      150                      155                      160
151 His Ser Tyr Asp Pro Trp Asp Pro Asn Tyr Arg His Ile Gly Ile Asp
152                      165                      170                      175
154 Val Asn Gly Ile Glu Ser Ile Lys Thr Val Gln Trp Asp Trp Ile Asn
155                      180                      185                      190
157 Gly Gly Val Ala Phe Ala Thr Ile Thr Tyr Leu Ala Pro Asn Lys Thr
158                      195                      200                      205
160 Leu Ile Ala Ser Leu Val Tyr Pro Ser Asn Gln Thr Ser Phe Ile Val
161                      210                      215                      220
163 Ala Ala Ser Val Asp Leu Lys Gly Ile Leu Pro Glu Trp Val Arg Val
164 225                      230                      235                      240
166 Gly Phe Ser Ala Ala Thr Gly Ala Pro Lys Ala Val Glu Thr His Asp
167                      245                      250                      255
169 Val Arg Ser Trp Ser Phe Thr Ser Thr Leu Glu Ala Asn Ser Pro Ala
170                      260                      265                      270
172 Asp Val Asp Asn Asn Val His Ile Ala Arg Tyr Thr Ala
173                      275                      280                      285
177 <210> SEQ ID NO: 3
178 <211> LENGTH: 32
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
184 primer
186 <400> SEQUENCE: 3
187 ccgggtacct gcactagtag atagatgagc tc 32
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 32
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
197 primer
199 <400> SEQUENCE: 4
200 gagctcatct atctactagt gcaggtaccc gg 32
203 <210> SEQ ID NO: 5

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## RAW SEQUENCE LISTING

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TIME: 09:28:22

Input Set : A:\62870702.APP

Output Set: N:\CRF4\06142006\J524970A.raw

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204 <211> LENGTH: 26
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
210     primer
212 <400> SEQUENCE: 5
213 ccaggtgaaa ctgctcgagt cagatg                                26
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 28
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
223     primer
225 <400> SEQUENCE: 6
226 tgggcaacta gttgcagtgt aacgtgcg                                28
229 <210> SEQ ID NO: 7
230 <211> LENGTH: 26
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
236     primer
238 <400> SEQUENCE: 7
239 catcataacg gttctggcaa atattc                                26
242 <210> SEQ ID NO: 8
243 <211> LENGTH: 24
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
249     primer
251 <400> SEQUENCE: 8
252 gttaatagca tctctagttt accc                                24
255 <210> SEQ ID NO: 9
256 <211> LENGTH: 59
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
262     primer
264 <220> FEATURE:
265 <221> NAME/KEY: modified_base
266 <222> LOCATION: (34)..(35)
267 <223> OTHER INFORMATION: a, c, g, t, or u
269 <400> SEQUENCE: 9
W--> 270 ctacaagatc taacatcgtg ggtttcaact gcmnnttttag gagcaccctg ggcagcaga 59
273 <210> SEQ ID NO: 10

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## RAW SEQUENCE LISTING

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Input Set : A:\62870702.APP

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274 <211> LENGTH: 59
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
280     primer
282 <220> FEATURE:
283 <221> NAME/KEY: modified_base
284 <222> LOCATION: (37)..(38)
285 <223> OTHER INFORMATION: a, c, g, t, or u
287 <400> SEQUENCE: 10
W--> 288 ctacaagatc taacatcgtg gggtttcaact gctttmnnag gagcaccgt ggcagcaga 59
291 <210> SEQ ID NO: 11
292 <211> LENGTH: 59
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
298     primer
300 <220> FEATURE:
301 <221> NAME/KEY: modified_base
302 <222> LOCATION: (40)..(41)
303 <223> OTHER INFORMATION: a, c, g, t, or u
305 <400> SEQUENCE: 11
W--> 306 ctacaagatc taacatcgtg gggtttcaact gctttaggmn nagcaccgt ggcagcaga 59
309 <210> SEQ ID NO: 12
310 <211> LENGTH: 59
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
316     primer
318 <220> FEATURE:
319 <221> NAME/KEY: modified_base
320 <222> LOCATION: (44)..(45)
321 <223> OTHER INFORMATION: a, c, g, t, or u
323 <400> SEQUENCE: 12
W--> 324 ctacaagatc taacatcgtg gggtttcaac tgcttttagga gcmnnaccgt ggcagcaga 59
327 <210> SEQ ID NO: 13
328 <211> LENGTH: 59
329 <212> TYPE: DNA
330 <213> ORGANISM: Artificial Sequence
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
334     primer
336 <400> SEQUENCE: 13
337 ctacaagatc taacatcgtg gggtttcaaaa actgcttttag gagcaccgt ggcagcaga 59
340 <210> SEQ ID NO: 14
341 <211> LENGTH: 59

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/524,970A

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Input Set : A:\62870702.APP  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 34,35  
Seq#:10; N Pos. 37,38  
Seq#:11; N Pos. 40,41  
Seq#:12; N Pos. 44,45  
Seq#:32; N Pos. 19,20,22,23,28,29,31,32,37,38,40,41  
Seq#:37; Xaa Pos. 10  
Seq#:39; Xaa Pos. 4,5,7,8,10,11

## VERIFICATION SUMMARY

DATE: 06/14/2006

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Input Set : A:\62870702.APP

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L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0  
L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0  
L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0  
L:744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0